

**Amendments to the Specification:**

Please replace paragraph [0040] (and Table 1) beginning at page 14, line 8, with the following:

--[0040] An additional and effective way to reduce the complexity of a library is to divide the members of a protein family of interest into two or more sub-sets, each sub-set comprising members having a variant of the signature sequence, each such variant comprising a relatively high number of amino acids that are constant for all members of the sub-set. The effect of such division can be seen clearly with reference to Example 2 and Table 1 below, which shows the division into seven sub-sets of the 89 known members of the family of tyrosine kinases. Each of sub-sets 1 and 4-7 have a different variant of the signature motif, but all five comprise seven amino acids that are constant for all members of the respective sub-set. Sub-set 3 has a variant signature sequence in which only one of the seven amino acids is not constant for all members of the sub-set; and only sub-set 2 has a variant signature motif in which three of the amino acids are not constant for all members.

Table 1

Variant	Signature Motif	SEQ ID NO:	No. of Known Members	Complexity
1	H R D L K S S	282	3	4
2	H R N/D L/V/I A A/V R	283	3	2,304
3	H R D L R A/S A	284	8	10,368
4	H R/K D L A T R	285	9	2,592
5	H R D L A A R	286	61	8,192
6	H K D L A A R	287	3	576
7	H R D I A A R	288	2	<del>32</del> 64
Total			89	24,068 <u>24100</u>

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Please replace paragraph [0041] beginning on page 14 with the following substitute paragraph:

--[0041] As a consequence of this division of the family into seven sub-sets, and as a further consequence of the fact that only known codons are taken into account when translating

each of the variants of the signature motif into a consensus sequence, the total complexity of the library is significantly reduced. In the case of the family of tyrosine kinases, were an siRNA library to be produced without this division, the complexity of the library would be on the order of tens of millions of members. As can be seen from Table 1, when such a division into the seven sub-sets listed in the table is done, the effect is to enable the production of a library having only ~~24,068~~ 24,100 members. It will be appreciated that such a library is formed by combining all the DNA oligonucleotides synthesized on the basis of each of the seven consensus sequences and ligating these to the expression cassettes; in a preferred embodiment, in order to obtain a uniform complexity of ~~24,068~~ 24,100 members, the seven batches of oligonucleotides are mixed together in direct proportion to their complexity prior to incorporation in the cassettes.--